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#2

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/898,554

DATE: 07/23/2001

TIME: 13:49:31

Input Set : A:\898554.txt

Output Set: N:\CRF3\07232001\I898554.raw

ENTERED

3 <110> APPLICANT: TALL, ALAN R  
 4 WELCH, CARRIE L  
 5 LIANG, CHIEN-PING  
 7 <120> TITLE OF INVENTION: ATHEROSCLEROSIS SUSECPTIBILITY GENE LOCUS 1 ( ATHSQ1) AND  
 ATHEROSCLEROSIS

8 SUSCEPTIBILITY GENE LOCUS 2 (ATHSQ2)  
 10 <130> FILE REFERENCE: 0575/64077  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/898,554  
 C--> 12 <141> CURRENT FILING DATE: 2001-07-02

ENTERED

p. 5

12 <160> NUMBER OF SEQ ID NOS: 40  
 14 <170> SOFTWARE: PatentIn version 3.1  
 16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 25

18 <212> TYPE: DNA  
 19 <213> ORGANISM: Artificial Sequence ✓

21 <220> FEATURE:  
 22 <223> OTHER INFORMATION: Primer ✓

24 <400> SEQUENCE: 1  
 25 accccaagac gtgctcccag gatga

25

28 <210> SEQ ID NO: 2  
 29 <211> LENGTH: 24

30 <212> TYPE: DNA  
 31 <213> ORGANISM: Artificial Sequence ✓

33 <220> FEATURE:  
 34 <223> OTHER INFORMATION: Primer ✓

36 <400> SEQUENCE: 2  
 37 cgcagtgctc ctcacatctgac ttgt

24

40 <210> SEQ ID NO: 3  
 41 <211> LENGTH: 25

42 <212> TYPE: DNA  
 43 <213> ORGANISM: Artificial Sequence ✓

45 <220> FEATURE:  
 46 <223> OTHER INFORMATION: Primer ✓

48 <400> SEQUENCE: 3  
 49 aggatctcgt cgtgacccat ggcga

25

52 <210> SEQ ID NO: 4  
 53 <211> LENGTH: 26

54 <212> TYPE: DNA  
 55 <213> ORGANISM: Artificial Sequence ✓

57 <220> FEATURE:  
 58 <223> OTHER INFORMATION: Primer ✓

60 <400> SEQUENCE: 4  
 61 gagcgcgcat accgtaaagc acgagg

26

64 <210> SEQ ID NO: 5  
 65 <211> LENGTH: 17

66 <212> TYPE: DNA  
 67 <213> ORGANISM: Artificial Sequence ✓

69 <220> FEATURE:

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70 <223> OTHER INFORMATION: Primer ✓
72 <400> SEQUENCE: 5
73 tgtgctgatg caggcac 17
76 <210> SEQ ID NO: 6
77 <211> LENGTH: 20
78 <212> TYPE: DNA
79 <213> ORGANISM: Artificial Sequence ✓
81 <220> FEATURE:
82 <223> OTHER INFORMATION: Primer ✓
84 <400> SEQUENCE: 6
85 gagaggaatg ctggtaggca 20
88 <210> SEQ ID NO: 7
89 <211> LENGTH: 23
90 <212> TYPE: DNA
91 <213> ORGANISM: Artificial Sequence ✓
93 <220> FEATURE:
94 <223> OTHER INFORMATION: Primer ✓
96 <400> SEQUENCE: 7
97 gatgtcagaa tacagataca gca 23
100 <210> SEQ ID NO: 8
101 <211> LENGTH: 20
102 <212> TYPE: DNA
103 <213> ORGANISM: Artificial Sequence ✓
105 <220> FEATURE:
106 <223> OTHER INFORMATION: Primer ✓
108 <400> SEQUENCE: 8
109 gttgcagtgg caccctttaa 20
112 <210> SEQ ID NO: 9
113 <211> LENGTH: 30
114 <212> TYPE: DNA
115 <213> ORGANISM: Artificial Sequence ✓
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Primer ✓
120 <400> SEQUENCE: 9
121 atgacttttg atgacaagat gaagcctgcg 30
124 <210> SEQ ID NO: 10
125 <211> LENGTH: 30
126 <212> TYPE: DNA
127 <213> ORGANISM: Artificial Sequence ✓
129 <220> FEATURE:
130 <223> OTHER INFORMATION: Primer ✓
132 <400> SEQUENCE: 10
133 cttctcatgg tcttctccag aatctttaga 30
136 <210> SEQ ID NO: 11
137 <211> LENGTH: 1092
138 <212> TYPE: DNA
139 <213> ORGANISM: Murinae gen. sp.
141 <220> FEATURE:
142 <221> NAME/KEY: misc_feature

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143 &lt;223&gt; OTHER INFORMATION: B-Isoform 1

146 &lt;400&gt; SEQUENCE: 11

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147 atgacttttg atgacaagat gaagcctgcg aatgacgagc ctgatcagaa gtcattgtggc      60
149 aagaagccta aaggtctgca tttgttttct tccccatggt gggtccctgc tgctatgact      120
151 ctggtcatcc tctgcctggt gttgtcagtg acccttattg tacagtggac acaattacgc      180
153 caggtatctg acctcttaaa acaataccaa gcgaacctta ctcagcagga tcgtatcctg      240
155 gaagggcaga tgtagccca gcagaaggca gaaaacactt cacaggaatc aaagaaggaa      300
157 ctgaaaggaa agatagacac cctcaccag aagctgaacg agaaatccaa agagcaggag      360
159 gagcttctac agaagaatca gaacctccaa gaagccctgc aaagagctgc aaactcttca      420
161 gaggagtccc agagagaact caagggaag atagacacca tcaccggaa gctggacgag      480
163 aaatccaaag agcaggagga gcttctcag atgattcaga acctccaaga agccctgcag      540
165 agagctgcaa actcttcaga ggagtcccag agagaactca agggaaagat agacaccctc      600
167 accttgaagc tgaacgagaa atccaaagag caggaggagc ttctacagaa gaatcagaac      660
169 ctccaagaag ccctgcaaag agctgcaaac ttttcaggtc cttgtccaca agactggctc      720
171 tggcataaag aaaactgtta cctcttccat gggcccttta gctgggaaaa aaaccggcag      780
173 acctgccaat ctttgggtgg ccagttacta caaattaatg gtgcagatga tctgacattc      840
175 atcttacaag caatttccca taccacctcc ccgttctgga ttggattgca tcggaagaag      900
177 cctggccaac catggctatg ggagaatgga actccttga attttcaatt ctttaagacc      960
179 aggggcgttt ctttacagct actccttga attttcaatt ctttaagacc aggggcgttt     1020
181 ctttacagct aaaactgcat tctaattgca ttcagcatat gtcagaagaa gacaaatcat     1080
183 ttgcaaattt ag                                     1092

```

186 &lt;210&gt; SEQ ID NO: 12

187 &lt;211&gt; LENGTH: 1192

188 &lt;212&gt; TYPE: DNA

189 &lt;213&gt; ORGANISM: Murinae gen. sp.

191 &lt;220&gt; FEATURE:

192 &lt;221&gt; NAME/KEY: misc\_feature

193 &lt;223&gt; OTHER INFORMATION: M-Isoform 1

196 &lt;400&gt; SEQUENCE: 12

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197 atgacttttg atgacaagat gaagcctgcg aatgacgagc ctgatcagaa gtcattgtggc      60
199 aagaagccta aaggtctgca tttgttttct tccccatggt gggtccctgc tgctatgact      120
201 ctggtcatcc tctgcctggt gttgtcagtg acccttattg tacagtggac acaattacgc      180
203 caggtatctg acctcttaaa acaataccaa gcgaacctta ctcagcagga tcgtatcctg      240
205 gaagggcaga tgtagccca gcagaaggca gaaaacactt cacaggaatc aaagaaggaa      300
207 ctgaaaggaa agatagacac cctcaccag aagctgaacg agaaatccaa agagcaggag      360
209 gagcttctac agaagaatca aagctgaacg agaaatccaa agagcaggag gagcttctac      420
211 agaagaatca gaacctccaa gaagccctgc aaagagctgc aaactcttca gaggagtccc      480
213 gaacctccaa gaagccctgc aaagagctgc aaactcttca gaggagtccc agagagaact      540
215 caagggaag atagacacca tcaccggaa gctggacgag aaatccaaag agcaggagga      600
217 gcttctgcag atgattcaga acctccaaga agccctgcag agagctgcaa actcttcaga      660
219 ggagtcccag agagaactca agggaaagat agacaccctc accttgaagc tgaacgagaa      720
221 atccaaagag caggaggagc ttctacagaa gaatcagaac ctccaagaag ccctgcaaag      780
223 agctgcaaac ttttcaggtc cttgtccaca agactggctc tggcataaag aaaactgtta      840
225 cctcttccat gggcccttta gctgggaaaa aaaccggcag acctgccaat ctttgggtgg      900
227 ccagttacta caaattaatg gtgcagatga tctgacattc atcttacaag caatttccca      960
229 taccacctcc ccattctgga ttggattgca tcggaagaag cctggccaac catggctatg     1020
231 ggagaatgga actccttga attttcaatt ctttaagacc aggggcgttt ctttacagct     1080
233 atattcatga gccaactgtg cataccttca agacggagct gtgttcgctg aaaactgcat     1140
235 tctaattgca ttcagcatat gtcagaagaa gacaaatcat ttgcaaattt ag               1192

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238 <210> SEQ ID NO: 13
239 <211> LENGTH: 744
240 <212> TYPE: DNA
241 <213> ORGANISM: Murinae gen. sp.
243 <220> FEATURE:
244 <221> NAME/KEY: CDS
245 <222> LOCATION: (1)..(744)
246 <223> OTHER INFORMATION:
249 <220> FEATURE:
250 <221> NAME/KEY: misc_feature
251 <223> OTHER INFORMATION: Isoform 7
254 <400> SEQUENCE: 13
255 atg act ttt gat gac aag atg aag cct gcg aat gac gag cct gat cag      48
256 Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln
257 1          5          10          15
259 aag tca tgt ggc aag aag cct aaa gag gag tcc cag aga gaa ctc aag      96
260 Lys Ser Cys Gly Lys Lys Pro Lys Glu Glu Ser Gln Arg Glu Leu Lys
261          20          25          30
263 gga aag ata gac acc atc acc cgg aag ctg gac gag aaa tcc aaa gag      144
264 Gly Lys Ile Asp Thr Ile Thr Arg Lys Leu Asp Glu Lys Ser Lys Glu
265          35          40          45
267 cag gag gag ctt ctg cag atg att cag aac ctc caa gaa gcc ctg cag      192
268 Gln Glu Glu Leu Leu Gln Met Ile Gln Asn Leu Gln Glu Ala Leu Gln
269          50          55          60
271 aga gct gca aac tct tca gag gag tcc cag aga gaa ctc aag gga aag      240
272 Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln Arg Glu Leu Lys Gly Lys
273 65          70          75          80
275 ata gac acc ctc acc ttg aag ctg aac gag aaa tcc aaa gag cag gag      288
276 Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser Lys Glu Gln Glu
277          85          90          95
279 gag ctt cta cag aag aat cag aac ctc caa gaa gcc ctg caa aga gct      336
280 Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala Leu Gln Arg Ala
281          100          105          110
283 gca aac ttt tca ggt cct tgt cca caa gac tgg ctc tgg cat aaa gaa      384
284 Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu Trp His Lys Glu
285          115          120          125
287 aac tgt tac ctc ttc cat ggg ccc ttt ggc tgg gaa aaa aac cgg cag      432
288 Asn Cys Tyr Leu Phe His Gly Pro Phe Gly Trp Glu Lys Asn Arg Gln
289          130          135          140
291 acc tgc caa tct ttg ggt ggc cag tta cta caa att aat ggt gca gat      480
292 Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile Asn Gly Ala Asp
293 145          150          155          160
295 gat ctg aca ttc atc tta caa gca att tcc cat acc acc tcc cca ttc      528
296 Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr Thr Ser Pro Phe
297          165          170          175
299 tgg att gga ttg cat cgg aag aag cct ggc caa cca tgg cta tgg gag      576
300 Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro Trp Leu Trp Glu
301          180          185          190
303 aat gga act cct ttg aat ttt caa ttc ttt aag acc agg ggc gtt tct      624

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304 Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr Arg Gly Val Ser
305      195      200      205
307 tta cag cta tat tca tca agc aac tgt gca tac ctt caa gac gga gct      672
308 Leu Gln Leu Tyr Ser Ser Ser Asn Cys Ala Tyr Leu Gln Asp Gly Ala
309      210      215      220
311 gtg ttc gct gaa aac tgc att cta att gca ttc agc ata tgt cag aag      720
312 Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser Ile Cys Gln Lys
313 225      230      235      240
315 aag aca aat cat ttg caa att tag      744
316 Lys Thr Asn His Leu Gln Ile
317      245
320 <210> SEQ ID NO: 14
321 <211> LENGTH: 247
322 <212> TYPE: PRT
323 <213> ORGANISM: Murinae gen. sp.
325 <220> FEATURE:
326 <221> NAME/KEY: misc_feature
327 <223> OTHER INFORMATION: Isoform 7
329 <400> SEQUENCE: 14
331 Met Thr Phe Asp Asp Lys Met Lys Pro Ala Asn Asp Glu Pro Asp Gln
332 1      5      10      15
335 Lys Ser Cys Gly Lys Lys Pro Lys Glu Glu Ser Gln Arg Glu Leu Lys
336      20      25      30
339 Gly Lys Ile Asp Thr Ile Thr Arg Lys Leu Asp Glu Lys Ser Lys Glu
340      35      40      45
343 Gln Glu Glu Leu Leu Gln Met Ile Gln Asn Leu Gln Glu Ala Leu Gln
344      50      55      60
347 Arg Ala Ala Asn Ser Ser Glu Glu Ser Gln Arg Glu Leu Lys Gly Lys
348 65      70      75      80
351 Ile Asp Thr Leu Thr Leu Lys Leu Asn Glu Lys Ser Lys Glu Gln Glu
352      85      90      95
355 Glu Leu Leu Gln Lys Asn Gln Asn Leu Gln Glu Ala Leu Gln Arg Ala
356      100      105      110
359 Ala Asn Phe Ser Gly Pro Cys Pro Gln Asp Trp Leu Trp His Lys Glu
360      115      120      125
363 Asn Cys Tyr Leu Phe His Gly Pro Phe Gly Trp Glu Lys Asn Arg Gln
364      130      135      140
367 Thr Cys Gln Ser Leu Gly Gly Gln Leu Leu Gln Ile Asn Gly Ala Asp
368 145      150      155      160
371 Asp Leu Thr Phe Ile Leu Gln Ala Ile Ser His Thr Thr Ser Pro Phe
372      165      170      175
375 Trp Ile Gly Leu His Arg Lys Lys Pro Gly Gln Pro Trp Leu Trp Glu
376      180      185      190
379 Asn Gly Thr Pro Leu Asn Phe Gln Phe Phe Lys Thr Arg Gly Val Ser
380      195      200      205
383 Leu Gln Leu Tyr Ser Ser Ser Asn Cys Ala Tyr Leu Gln Asp Gly Ala
384      210      215      220
387 Val Phe Ala Glu Asn Cys Ile Leu Ile Ala Phe Ser Ile Cys Gln Lys
388 225      230      235      240

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Use of n and / or Xaa has been detected in the  
Sequence Listing. Review the Sequence Listing  
to ensure a corresponding explanation is present  
in the <220> to <223> fields of each sequence  
using R or Xaa.

## VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39

L:1506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39

L:1510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39

L:1638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40

L:1642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40

L:1646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40